

Result	No.	Score	% Match	Query Length	DB Length	ID	Description
c	1	925	100.0	925	14	US-10-039-836A-3	Sequence 3, Appli
c	2	59.6	6.4	925	14	US-10-039-836A-3	Sequence 3, Appli
c	3	45.8	5.0	10338	12	US-10-311-455-1518	Sequence 1518, Ap
c	4	44	4.8	3673778	12	US-10-312-841-2	Sequence 2, Appl
c	5	43.6	4.7	9524	12	US-10-311-455-812	Sequence 812, App
c	6	42.6	4.6	18817	12	US-10-240-485-48	Sequence 48, Appl
c	7	42.2	4.6	10254	12	US-10-311-455-1048	Sequence 1048, Ap
c	8	41.6	4.5	7676	12	US-10-240-485-152	Sequence 152, App
c	9	41.4	4.5	17594	12	US-10-311-455-1399	Sequence 1399, Ap
c	10	41.2	4.5	6275	12	US-10-311-455-524	Sequence 524, App
c	11	41	4.4	5488	12	US-10-311-455-1429	Sequence 1429, Ap
c	12	41	4.4	5930	12	US-10-311-455-1368	Sequence 1368, Ap
c	13	40.8	4.4	88	12	US-10-270-839-108	Sequence 108, App
c	14	40.6	4.4	2000	10	US-09-938-842A-5309	Sequence 5309, Ap
c	15	40.6	4.4	5487	12	US-10-311-455-1571	Sequence 1571, Ap
c	16	40.6	4.4	9927	12	US-10-311-455-85	Sequence 85, Appl

```

; LENGTH: 925
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Proteinase Inhibitor-like promoter
US-10-039-836A-3

Query Match      6.4%; Score 59.6; DB 14; Length 925;
Best Local Similarity 59.0%; Pred. No. 4.5e-05;
Matches 138; Conservative 0; Mismatches 94; Indels 2; Gaps 2;

QY 243 AAATTATTGGCCACTTAAGGAGGTGTTTGAATGCAATAAACTAATAGTAGTCTGGCTAA 302
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 475 AAATCAACGCTAGACTTATGCCATGTTTGAATGCAATAAACTAATAGTAGTCTGGCTAA 417
QY 303 AATTGTTAGTGAATATCTAGCTACAAATAGCTACCTAATTAATTAATTAATTAATTA 362
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 416 AATTAGTTGAGACATTCAACACAGCCCACTTAATAATTAATTAATTAATTAATTAATTA 357
QY 363 AAATAACTTATAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 422
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 356 AATTAGTTAATAGTATAGTATGTTTGTAGTAGATAATTTCACTAACAATTTTAGCC 297
QY 423 -ACTAAGTTTATCTTTAGTGCATTCACACATGCGCATAGCTACGTTTGTGATT 475
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 296 AACTAAGTATTAGTTTATTTAGTGCATTCACACATGCGCATAGCTACGTTTGTGATT 243

RESULT 3
US-10-311-455-1518
; Sequence 1518, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by D
; FILE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT FILING DATE: 2002-12-16
; PRIOR FILING DATE: 2001-07-02
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1518
; LENGTH: 10328
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1518

Query Match      5.0%; Score 45.8; DB 12; Length 10328;
Best Local Similarity 46.2%; Pred. No. 0.55;
Matches 152; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

QY 192 TTCCTCTTCTGCGCAGCTGTTTCTACATTTTCATTGGCAGATATGATGAACATAATTTG 251
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2221 TTTTATTTTATTTATATATAAAATTAACGTAAGATAAATTAAGATTTAAATTAAGA 2280
QY 252 GCCACTTAAGAGGTGTTTGAATGCAATAAACTAATAGTGTAGTCTGGCTAAATTTAG 311
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2281 TTTTAAATTTATAATTAATTTAGAGGAAAGGAAATATTTATTTGGAATTTATCTTTG 2340
QY 312 TGAATTTATCTAGCTACAAATAGCTACCTAATTAATTAATTAATTAATTAATTAATTA 371
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2341 GTAGAGAATTAGGATTAATTTTAAAGTAGTCTTAAAGGAAATTTAAAGTAAAGT 2400

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; LENGTH: 925
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Proteinase Inhibitor-like promoter
US-10-039-836A-3/C

Query Match      5.0%; Score 45.8; DB 12; Length 10328;
Best Local Similarity 46.2%; Pred. No. 0.55;
Matches 152; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

QY 192 TTCCTCTTCTGCGCAGCTGTTTCTACATTTTCATTGGCAGATATGATGAACATAATTTG 251
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2221 TTTTATTTTATTTATATATAAAATTAACGTAAGATAAATTAAGATTTAAATTAAGA 2280
QY 252 GCCACTTAAGAGGTGTTTGAATGCAATAAACTAATAGTGTAGTCTGGCTAAATTTAG 311
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2281 TTTTAAATTTATAATTAATTTAGAGGAAAGGAAATATTTATTTGGAATTTATCTTTG 2340
QY 312 TGAATTTATCTAGCTACAAATAGCTACCTAATTAATTAATTAATTAATTAATTAATTA 371
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2341 GTAGAGAATTAGGATTAATTTTAAAGTAGTCTTAAAGGAAATTTAAAGTAAAGT 2400

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```

; LENGTH: 925
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Proteinase Inhibitor-like promoter
US-10-039-836A-3/C

Query Match      5.0%; Score 45.8; DB 12; Length 10328;
Best Local Similarity 46.2%; Pred. No. 0.55;
Matches 152; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

QY 192 TTCCTCTTCTGCGCAGCTGTTTCTACATTTTCATTGGCAGATATGATGAACATAATTTG 251
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2221 TTTTATTTTATTTATATATAAAATTAACGTAAGATAAATTAAGATTTAAATTAAGA 2280
QY 252 GCCACTTAAGAGGTGTTTGAATGCAATAAACTAATAGTGTAGTCTGGCTAAATTTAG 311
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2281 TTTTAAATTTATAATTAATTTAGAGGAAAGGAAATATTTATTTGGAATTTATCTTTG 2340
QY 312 TGAATTTATCTAGCTACAAATAGCTACCTAATTAATTAATTAATTAATTAATTAATTA 371
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2341 GTAGAGAATTAGGATTAATTTTAAAGTAGTCTTAAAGGAAATTTAAAGTAAAGT 2400

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Qy	372	ATAGTTAAATATTATTAAGTTGGGTGTTTGAATGTCACAATAATTTAGCCACTAACTTT	431
Db	2401	GGGTTTAAATTAATTAAGATTTTGTATTGTTAAATAAATATTATTAAGAAAGTTAAATA	2460
Qy	432	TATCTTTAGTCGCTATCAACATGGCATACTACGTTGATTTGACAGCGTAGCATCGT	491
Db	2461	TATTAATTTATGGAATGGGAGGAATATTGTAAACGATGATTTGATTAAGGTTTAATATT	2520
Qy	492	CGGTACGGAAGAGGAACCAAGGATTTT	520
Db	2521	TCGAATTTATTAAGGATTTTAAATAAATGTT	2549


```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1999

Query Match      4.5%; Score 41.4; DB 12; Length 17594;
Best Local Similarity 51.5%; Pred. No. 9.8;
Matches 119; Conservative 0; Mismatches 111; Indels 1; Gaps 1;

QY 212 TCTACATTCATCGGCAGATATGATGACATAAATTTATGGCCACCTAAGGAGGTGTTG 271
Db 845 TGTATATATAGTTTAAATATATATAATAAATTTATAAATTTGATAAATTAAGTAAAGTGTGTT 904
QY 272 AATGCAATAAACTAATAGTCTAGCTGCTAAATTTCTAGTGAATTAATCTAGCTAACAA 331
Db 905 GATTTAATAAATAATAGATATTTAGTTAAATTTTAAATTTTAAATAATAGTATAATTT 964
QY 332 ATAGC-TACTACTACTAATTAACCAAAATAACTTATAGTTAAATTTAATTAAGTT 390
Db 965 TTAGGATAAGTATGTTATAAATTTCTATGGAATATATAAATAAATTTATTTCGTTT 1024
QY 391 GGGCTGTTTCAATGCTCACTAAATTTTAGCCCACTAATCTTTATCTTTAGT 441
Db 1025 TTGAAATTTAAATTTAGTCTAGTATTTTGTATTTTATTTGGGAAATTTAAT 1075

RESULT 10
US-10-311-455-524/c
; Sequence 524, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determination of Cytosine Methylation
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 524
; LENGTH: 6275
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-524

Query Match      4.5%; Score 41.2; DB 12; Length 6275;
Best Local Similarity 52.3%; Pred. No. 6.4;
Matches 91; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 279 TAAACTAATAGTTAGTTGGCTAAATTTCTTAGTGAATTTATCTAGCTAACAAATAGCTA 338
Db 3387 TAAATAAATTTAAACTTTAAATAACATTTTATTTAAATCTCTTTTAAATAAATATATA 3328
QY 339 CTTAACTATTAACTAATTTACCAAAATAAATATATAGTTAAATTTATTAAGTTGGGCTGTT 398
Db 3327 CAAAAATATTTTACATACATAAATAATATACCTCTCTTTTAACTCTACATTTCTTAAT 3268
QY 399 TGAATGCTCACTAATTTTAGCCCACTAATCTTTTATCTTTTAGTGCAATTCACAA 452
Db 3267 TTTATATCAAAACATTTTAAACAAACAAACAACTATCCCTAAATCATATAAACA 3214

RESULT 11
US-10-311-455-1429
```

```
; Sequence 1429, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determination of Cytosine Methylation
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1429
; LENGTH: 5488
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1429

Query Match      4.4%; Score 41; DB 12; Length 5488;
Best Local Similarity 55.2%; Pred. No. 6.8;
Matches 80; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 302 AAATGTTAGTGAATTAATCTAGCTAACAAATAGCTACCTAATTAATTAATTAATTAATTA 361
Db 1615 AAATGATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1674
QY 362 AAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 421
Db 1675 AATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1734
QY 422 CACTAATCTTTATCTTTAGTGCAAT 446
Db 1735 ATTTATTTATTTATTTAGTGTTT 1759

RESULT 12
US-10-311-455-1368/c
; Sequence 1368, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determination of Cytosine Methylation
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1368
; LENGTH: 5930
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1368

Query Match      4.4%; Score 41; DB 12; Length 5930;
Best Local Similarity 49.8%; Pred. No. 7;
```

```
Matches 104: Conservative 0; Mismatches 105; Indels 0; Gaps 0;
QY 230 ATATGTGTAAGTAATTTATGGCCACTTACGAGGCTTTGAATGCAATFAAACTAATA 289
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5093 AAATTTAAACTAAATTCCTAAATCTAAATATATTAATTAATTAATAATAAA 5034
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 290 GTTAGTTGGCTAAATTTAGTGAATTTACTAGCTAAACAATAGCTACCTAACTATTA 349
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5033 AATAAAAACTTTCATTTTACTTTATTTCTATACTTTAAAAAATACTTAAAAACGTATA 4974
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 350 ACTAATTTACCAAAATACTTATAGTTAAATTAATTAAGTTGGCTGTTTGAATGCTCA 409
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4973 TTATTTTATATAAATACATTTAATACAAAATTTCAAATATTACTTTTCTCAACAAATT 4914
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 410 ACTAATTTAGCCACTAACTTTTATCTTT 438
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4913 ACAATTTAAACTTTAAATTTTTTTTATT 4885
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
US-10-839-108/c
; Sequence 108, Application US/10270839
; Publication No. US20030143586A1
; GENERAL INFORMATION:
; APPLICANT: Chao, Qimin
; APPLICANT: Grasso, Luigi
; APPLICANT: Sass, Philip M.
; APPLICANT: Nicolaides, Nicholas C.
; TITLE OF INVENTION: Genetic Hypermutability of Plants for Gene Discovery and Diagnosis
; FILE REFERENCE: AG000205 (MOR-0133)
; CURRENT APPLICATION NUMBER: US/10/270,839
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/328,750
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 88
; TYPE: DNA
; ORGANISM: Conyza sp.
US-10-270-839-108

Query Match 4.4%; Score 40.8; DB 12; Length 88;
Best Local Similarity 75.0%; Pred. No. 0.88;
Matches 51; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 1 ACTATAGGCGACGGTGTGCGAGCGCCGGCTGCTGATTTGTGTGTCACCAACTTTGA 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 88 ACTAAAGGCGACGGTGTGCGAGCGCCGGCTGCTGATTTGTGTGTCACCAACTTAT 29
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 TGTGATGG 68
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 28 TCAGATCG 21
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
US-09-938-842A-5309/c
; Sequence 5309, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
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; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 5309
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-5309

Query Match 4.4%; Score 40.6; DB 10; Length 2000;
Best Local Similarity 50.8%; Pred. No. 5.1;
Matches 97; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
QY 215 ACATTTTCATGGCAGATATGTATGAATTAATTTGCCCACTTAAGGAGGTGTTGAAT 274
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1728 ATATATATATGGATAATGAGAACTGACTTATATAGATATAATTAAGTTTATGAT 1669
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 275 GCAATAAACTAATAGTTAGTTGGCTAAATTTGTTAGTGAATTTATCTAGCTACAATA 334
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1668 TCAATCAATTAATAATATATATACTTAATAAATTTAAATTTATCTATATAATAA 1609
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 335 GCTACCTAATTAATTAATTTACCAAAATACTTAACTTAAATTTAACTTAACTTGGC 394
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1608 TTTTGCATGTAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1549
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 395 TGTTTGAATGT 405
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1548 TATTTGATTTCT 1538
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
US-10-311-455-1571
; Sequence 1571, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by D
; TITLE OF INVENTION: Cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1571
; LENGTH: 5487
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1571

Query Match 4.4%; Score 40.6; DB 12; Length 5487;
Best Local Similarity 56.3%; Pred. No. 8.6;
Matches 76; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
QY 273 ATGCAATAAACTAATAGTTAGTTGGCTAAATTTGTTAGTGAATTTATCTAGCTACAAA 332
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 495 ATTTAATTTAAATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 554
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 333 TAGCTACCTAATTAATTAATTTACCAAAATACTTAACTTAAATTTAAATTTAAATTTAG 392
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 555 TATATAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 614
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 393 GCTGTTTGAATGCT 407
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 615 GATTATAAATTTT 629
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Fri Oct 17 11:56:06 2003

us-10-039-836a-3.rnpb

Page 7

Search completed: October 17, 2003, 11:44:17
Job time : 248 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 17, 2003, 08:56:08 ; Search time 64 Seconds
(without alignments)
6379.366 Million cell updates/sec

Title: US-10-039-836A-3
Perfect score: 925
Sequence: 1 actataggccagcgtgtgc.....ccgcagggaagaatctatc 925

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
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2: /cgn2.6/prodata/2/ina/5B_COMB.seq:*
3: /cgn2.6/prodata/2/ina/6A_COMB.seq:*
4: /cgn2.6/prodata/2/ina/6B_COMB.seq:*
5: /cgn2.6/prodata/2/ina/PTUS_COMB.seq:*
6: /cgn2.6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.8	10.9	4137	3	US-08-750-357-7
2	99	10.7	318	4	US-09-313-294A-7567
3	45.4	4.9	3618	1	US-07-872-678A-36
4	40.8	4.4	4137	3	US-08-750-357-7
5	40.4	4.4	763	4	US-09-276-595-14
6	39.6	4.3	269	4	US-09-313-294A-3328
7	39.6	4.3	6078	3	US-09-173-914-1
8	39	4.2	340	4	US-09-323-195A-3
9	39	4.2	615	3	US-08-998-416-186
10	39	4.2	1172	4	US-08-969-046-5
11	38.6	4.2	1308	4	US-09-601-198-3
12	38.2	4.1	1924	4	US-09-424-283-5
13	38	4.1	2791	4	US-09-570-367C-1
14	37.8	4.1	555	3	US-08-905-223-37
15	37.8	4.1	555	4	US-09-247-155-37
16	37.8	4.1	555	4	US-09-599-360B-23
17	37.8	4.1	555	4	US-09-663-600A-37
18	37.6	4.1	4526	4	US-09-424-283-7
19	37.6	4.1	9827	4	US-09-453-702B-66
20	37.6	4.1	53332	4	US-09-801-861-3
21	37.4	4.0	665	2	US-08-883-795A-36
22	37.2	4.0	1664976	4	US-08-916-421B-1
23	37	4.0	678	1	US-07-991-867B-23
24	37	4.0	678	1	US-08-107-755A-23
25	37	4.0	678	2	US-08-544-332-23
26	37	4.0	678	4	US-09-370-861A-23
27	37	4.0	3718	4	US-09-424-283-6

Sequence 1, Appli
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Sequence 1, Appli
Sequence 36, Appli
Sequence 5, Appli
Sequence 13, Appli
Sequence 1, Appli
Sequence 18, Appli
Sequence 35, Appli
Sequence 5, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 178, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
US-08-107-755A-1
US-07-991-867B-1
US-08-544-332-1
US-09-370-861A-1
US-09-402-532-38
US-09-323-195A-5
US-09-276-599-13
US-08-545-528D-1
US-08-913-014A-18
US-09-402-532-35
US-09-257-583-5
US-09-323-195A-1
US-09-377-648-4
US-09-383-543A-4
US-09-601-198-178
US-09-004-056-1
US-09-570-367C-1
US-09-734-674-1

ALIGNMENTS

RESULT 1
US-08-750-357-7
Sequence 7, Application US/08750357
Patent No. 6008437
GENERAL INFORMATION:
APPLICANT: KREBBERS, Enno
APPLICANT: WILLIAMS, Mark
APPLICANT: LEEMANS, Jan
TITLE OF INVENTION: USE OF ANTHOCYANIN GENES TO MAINTAIN
TITLE OF INVENTION: MALE STERILE PLANTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,357
FILING DATE: 21-MAR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 018030-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4137 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: E. coli-HindIII region of plasmid pCOL13
FEATURE:
NAME/KEY: prim_transcript
LOCATION: 188
FEATURE:
NAME/KEY: exon
LOCATION: 188...212
FEATURE:

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; NAME/KEY: intron
; LOCATION: 213..556
; FEATURE:
; NAME/KEY: exon
; LOCATION: 557..718
; FEATURE:
; NAME/KEY: intron
; LOCATION: 719..1224
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1226..2771
; OTHER INFORMATION: /codon_start= 2
; OTHER INFORMATION: /note= "exon containing 3' end coding region of B-peru gene.
; OTHER INFORMATION: This exon continues up to the polyadenylation site."
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 576..718
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1226..2771
; FEATURE:
; NAME/KEY:
; LOCATION: 1269..2771
; OTHER INFORMATION: /note= "fragment of B-peru coding
; OTHER INFORMATION: region which is derived from cDNA"
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 2772..4137
; FEATURE:
; NAME/KEY:
; LOCATION: 1..6
; OTHER INFORMATION: /label= EcoRI
; NAME/KEY:
; LOCATION: 11..16
; OTHER INFORMATION: /label= XbaI
; FEATURE:
; NAME/KEY:
; LOCATION: 45..50
; OTHER INFORMATION: /label= KpnI
; FEATURE:
; NAME/KEY:
; LOCATION: 265..270
; OTHER INFORMATION: /label= HindIII
; FEATURE:
; NAME/KEY:
; LOCATION: 329..334
; OTHER INFORMATION: /label= XbaI
; FEATURE:
; NAME/KEY:
; LOCATION: 835..840
; OTHER INFORMATION: /label= BamHI
; FEATURE:
; NAME/KEY:
; LOCATION: 1269..1274
; OTHER INFORMATION: /label= MluI
; FEATURE:
; NAME/KEY:
; LOCATION: 2788..2793
; OTHER INFORMATION: /label= HindIII
; FEATURE:
; NAME/KEY:
; LOCATION: 2884..2889
; OTHER INFORMATION: /label= MluI
; FEATURE:
; NAME/KEY:
; LOCATION: 2828..2833
; OTHER INFORMATION: /label= HindIII
; FEATURE:
; NAME/KEY:
; LOCATION: 4114..4119
; OTHER INFORMATION: /label= SalI
; FEATURE:
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; NAME/KEY:
; LOCATION: 4132..4137
; OTHER INFORMATION: /label= HindIII
; FEATURE:
; NAME/KEY:
; LOCATION: 4114..4137
; OTHER INFORMATION: /label= polylinker
; OTHER INFORMATION: /note= "part of polylinker of pUC19"
; US-08-750-357-7

Query Match
Best Local Similarity 10.9%; Score 100.8; DB 3; Length 4137;
Matches 156; Conservative 0; Mismatches 72; Indels 2; Gaps 1;

Qy 262 GAGGTGTTGAATGCAATAAACTAATAGTAGTTGGCT--AAATTTGTTAGTGAATTA 319
Db 3332 GAGGTGTTGAATGCAATAAACTAATAGTAGTTGGCTTAAATAATTAATAAATTA 3391
Qy 320 TCTAGCTAACAAATAGCTACCTAACTAATTAACCTAATTAACCAAAATAACTATATAGTTAA 379
Db 3392 GTTAGTTAATAATAGCTAGCTAAATATAGCTAAATTTGTCAAAAGTAGCTAATAGCTGA 3451
Qy 380 ATTATTAAAGTTGGCTGTTTGAATGCTCAACTAATTTTACCACTAACTTTTATCTTTA 439
Db 3452 ATTATTAGCTATATTGTTTGAATGCTCTCAGCTAATTTTACGAGATCATTTATTAGTTCTA 3511
Qy 440 GTGCATTCAACACATGGCATAAGCTAGCTTTGATTTGAGACGGTAGCATC 489
Db 3512 GTGTATCTAACACACCCCTTAGTCAACATGGTAAAAAAGTTGATTC 3561

RESULT 2
US-09-313-294A-7567/C
; Sequence 7567, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 7567
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700381949H1
; NAME/KEY: unsure
; LOCATION: 101,104,234,255,258,268,280,285-286,289,297,314
; OTHER INFORMATION: a, t, c, g, or other
; US-09-313-294A-7567

Query Match
Best Local Similarity 10.7%; Score 99; DB 4; Length 318;
Matches 122; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

Qy 258 TAAGGAGGTGTTTGAATGCAATAAACTAATAGTAGTTGGCT-AAAATTTAGTGAATA 316
Db 144 TAAAGGGGTGTTTGAATGCAATAAACTAATAGTAGTTGGCTTAAATAATTAATAAATTA 85
Qy 317 TTATCTAGCTAACAAATAGCTACCTAACTAATTAACCTAATTAACCAAAATAACTTATAGT 376
Db 84 TTAGCTAGCTAACAAATAGCTACCTAACTAATTAACCTAATTAACCAAAATAACTTATAGT 25
Qy 377 TAAATTAATAGTTGGCTGTTTGG 400
Db 24 TCAACTATTAGCTAGGTGTTGG 1
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RESULT 3

US-07-872-678A-36/c
; Sequence 36, Application US/07872678A
; Patent No. 5541060
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme, et al.
; TITLE OF INVENTION: DETECTION OF EARLY-ONSET
; TITLE OF INVENTION: NON-INSULIN-DEPENDENT DIABETES MELLITUS
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: Post Office Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/872,678A
; FILING DATE: 22-APRIL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coughlin, Daniel F.
; REGISTRATION NUMBER: 36,111
; REFERENCE/DOCKET NUMBER: ARCD016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; TELEX: 79-0924

INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3618 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-872-678A-36

Query Match 4.9%; Score 45.4; DB 1; Length 3618;
Best Local Similarity 53.0%; Pred. No. 0.0038;
Matches 97; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY	257	TTAAGGAGGTGTTGAATGCAATAAATACTAATAGTAGTTGGCTAAATTTGTTAGTGAAA	316
Db	2959	TAAATTAATGCTTAAATTAACCTTAAATTTTAAATAATGTTAATAATTTTAAATAAT	2900
QY	317	TTATCTAGCTAACAAATAGCTACCTAATTAATTAATTAATTAATTAATTAATTAATTAAT	376
Db	2899	TTAATAATTTTAATAAATAATATGTTAAATTTAAATTTAAATTTAAATTTAAATTTAAAT	2840
QY	377	TAAATTTAATGTTGGGTGTTGAAATGCTCAACTAATTTTACCACTAATTTTATCT	436
Db	2839	TTTAAATATGTTAAATAATTTTAAATAAATTTAATAATTTAATAATTTAATAATGTTGGTATCTAT	2780
QY	437	TTA 439	
Db	2779	ATA 2777	

RESULT 4

US-08-750-357-7/c
; Sequence 7, Application US/08750357
; Patent No. 6008437
; GENERAL INFORMATION:

; APPLICANT: KREBBERS, Enno
; APPLICANT: WILLIAMS, Mark
; APPLICANT: LEEMANS, Jan
; TITLE OF INVENTION: USE OF ANTHOCYANIN GENES TO MAINTAIN

TITLE OF INVENTION: MALE STERILE PLANTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,357
; FILING DATE: 21-MAR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 018030-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4137 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Ecori-HindIII region of plasmid pCOLL3
; FEATURE:
; NAME/KEY: prim_transcript
; LOCATION: 188
; FEATURE:
; NAME/KEY: exon
; LOCATION: 188..212
; FEATURE:
; NAME/KEY: intron
; LOCATION: 213..556
; FEATURE:
; NAME/KEY: exon
; LOCATION: 557..718
; FEATURE:
; NAME/KEY: intron
; LOCATION: 719..1224
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1226..2771
; OTHER INFORMATION: /codon_start= 2
; OTHER INFORMATION: /note="exon containing 3' end coding region of B-peru ge
; OTHER INFORMATION: This exon continues up to the polyadenylation site."
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 576..718
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1226..2771
; FEATURE:
; NAME/KEY: -
; LOCATION: 1269..2771
; OTHER INFORMATION: /note="fragment of B-peru coding
; OTHER INFORMATION: region which is derived from cDNA"
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 2772..4137
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..6
; OTHER INFORMATION: /label= Ecori

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1 FEATURE:
2 NAME/KEY: -
3 LOCATION: 11..16
4 OTHER INFORMATION: /label= XbaI
5 FEATURE:
6 NAME/KEY: -
7 LOCATION: 45..50
8 OTHER INFORMATION: /label= KpnI
9 FEATURE:
10 NAME/KEY: -
11 LOCATION: 265..270
12 OTHER INFORMATION: /label= HindIII
13 FEATURE:
14 NAME/KEY: -
15 LOCATION: 329..334
16 OTHER INFORMATION: /label= XbaI
17 FEATURE:
18 NAME/KEY: -
19 LOCATION: 835..840
20 OTHER INFORMATION: /label= BamHI
21 FEATURE:
22 NAME/KEY: -
23 LOCATION: 1269..1274
24 OTHER INFORMATION: /label= MluI
25 FEATURE:
26 NAME/KEY: -
27 LOCATION: 2788..2793
28 OTHER INFORMATION: /label= HindIII
29 FEATURE:
30 NAME/KEY: -
31 LOCATION: 2884..2889
32 OTHER INFORMATION: /label= MunI
33 FEATURE:
34 NAME/KEY: -
35 LOCATION: 2828..2833
36 OTHER INFORMATION: /label= HindIII
37 FEATURE:
38 NAME/KEY: -
39 LOCATION: 4114..4119
40 OTHER INFORMATION: /label= SalI
41 FEATURE:
42 NAME/KEY: -
43 LOCATION: 4132..4137
44 OTHER INFORMATION: /label= HindIII
45 FEATURE:
46 NAME/KEY: -
47 LOCATION: 4114..4137
48 OTHER INFORMATION: /label= polylin
49 OTHER INFORMATION: /note= "part of
50 IS-08-750-357-7"

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[illegible]

RESULT 5

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US-09-276-599-14/C
; Sequence 14, Application US/09276599
; Patent No. 6380459
; GENERAL INFORMATION:
; APPLICANT: Perera, J. Ranjan
; APPLICANT: Rice, Stephen J.
; TITLE OF INVENTION: Composition and method
; TITLE OF INVENTION: modification of gene e
; FILE REFERENCE: 11000.1036
; CURRENT APPLICATION NUMBER: US/09/276.599
; CURRENT FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 763
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-276-599-14

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Query Match      4.4%; Score 40.4; DB 4; Length 763;
Best local Similarity 97.6%; Pred. NO. 0.054;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACTATAGGCACGGTGTGTCGACGGCCCGGGCTGTCGTATT 42
db 759 ACTATAGGCACGGTGTGTCGACGGCCCGGGCTGTCGTATT 718

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RESULT 6

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US-09-313-294A-3328
; Sequence 3328, Application US/09313294A
; Patent No. 6476212
;
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 3328
; LENGTH: 269
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No. 6476212 7006a11343H1
; NAME/KEY: unsure
; LOCATION: 266
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-3328

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Query Match	4.3s; Score 39.6; DB 4; Length 269;
Best Local Similarity	83.6%; Pred.No. 0.061;
Matches	56; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
QY	265 GGTGTTGAATGCAATAAACTAAATAGTTAGTTGGCT-AAAATTGTTAGTGAATAATATCTA 323
Db	201 GTGTTTGAATGCACACTAGAGATAATAGTTAGTTAGTAAAATAATGTTAGTGGAAATTAGCTA 260
QY	324 GCTAACAA 330
Db	261 GCTACGNA 267

RESULT 7

US-09-173-914-1
; Sequence 1, Application US/09173914
; Patent No. 6171857
; GENERAL INFORMATION:
; APPLICANT: Hendrickson, Eric

; TITLE OF INVENTION: A No. 6171857el Leucine zipper, KARP-1 and
; TITLE OF INVENTION: Methods of Regulating DNA Dependent Protein Kinase Activity
; FILE REFERENCE: B0877/7017/HK
; CURRENT APPLICATION NUMBER: US/09/173,914
; CURRENT FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 60/064,557
; EARLIER FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 6078
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (178)...(178)
; NAME/KEY: unsure
; LOCATION: (230)...(230)
; NAME/KEY: unsure
; LOCATION: (232)...(232)
; NAME/KEY: unsure
; LOCATION: (234)...(234)
; NAME/KEY: unsure
; LOCATION: (453)...(453)
; NAME/KEY: unsure
; LOCATION: (473)...(473)
; NAME/KEY: unsure
; LOCATION: (610)...(610)
; NAME/KEY: unsure
; LOCATION: (612)...(612)
; NAME/KEY: unsure
; LOCATION: (2175)...(2175)
; NAME/KEY: unsure
; LOCATION: (1014)...(1014)
US-09-173-914-1

Query Match 4.3%; Score 39.6; DB 3; Length 6078;
Best Local Similarity 83.3%; Pred. No. 0.2;
Matches 45; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ACTATAGGCACGGTGGTGCACGGCCGGCTGGTGTATTTGTGTCACAAACA 54
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Db 12 ACTATAGGCACGGTGGTGCACGGCCGGCTGGTGTATTTGTGTCACAAACA 65

RESULT 8

US-09-323-195A-3
; Sequence 3, Application US/09323195A
; Patent No. 6462257
; GENERAL INFORMATION:
; APPLICANT: Pullman, Gerald
; APPLICANT: Cairney, John
; APPLICANT: Periera, Ranjan
; TITLE OF INVENTION: VICILIN-LIKE SEED STORAGE PROTEIN GENE PROMOTER AND
; FILE REFERENCE: IPST0009
; CURRENT APPLICATION NUMBER: US/09/323,195A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 340
; TYPE: DNA
; ORGANISM: Pinus taeda
US-09-323-195A-3

Query Match 4.2%; Score 39; DB 4; Length 340;
Best Local Similarity 89.4%; Pred. No. 0.098;
Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACTATAGGCACGGTGGTGCACGGCCGGCTGGTGTATTTGTGT 47
|||||
Db 1 ACTATAGGCACGGTGGTGCACGGCCGGCTGGTGTATTTGTGT 47

RESULT 9

US-08-998-416-186
; Sequence 186, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Redischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPHII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cortwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 615 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1074RP
US-08-998-416-186

Query Match 4.2%; Score 39; DB 3; Length 615;
Best Local Similarity 50.8%; Pred. No. 0.12;
Matches 93; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 237 TGAACATAATTTGGCCACTTAAGGAGGTGTTTGAATGCAATAAACTAATAGTTAGTT 296
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Db 426 TGATTTATATTTTAACTTTTATAAGAATTTATTAATAATTTTAACTTTAATT 485
QY 297 GGCTAAATTTAGTGAATTTCTAGCTAACAAATAGCTAGCTAACTAATTAACAAATT 356
|||||
Db 486 TCTATTATTAAATTTTATATTTTAAATAATTTATTCATTTTATTATTATTATT 545
QY 357 TACCAAAATAACTTATAGTTAAATTTAAGTTGGCTCTTTGAATGCTCAACTAATT 416
|||||
Db 546 TAATTAATTAATTTATTTAATTTATTTATTTATTTATTTATTTAATAATAATAATTA 605
QY 417 TTA 419
|||
Db 606 TAA 608

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RESULT 10
US-08-969-046-5/c
; Sequence 5, Application US/08969046B
; Patent NO. 6455762
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent Lee C.
; APPLICANT: Tsai, Chung-Jui
; APPLICANT: Hu, Wen-Jing
; TITLE OF INVENTION: Genetic engineering of trees through
; manipulation of lignin biosynthesis
; FILE REFERENCE: 881.003051
; CURRENT APPLICATION NUMBER: US/08/969.046B
; CURRENT FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1172
; TYPE: DNA
; ORGANISM: Populus tremuloides Michx.
US-08-969-046-5

Query Match      4.2%; Score 39; DB 4; Length 1172;
Best Local Similarity 54.5%; Pred. No. 0.16;
Matches 78; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY      244  AATTAATGGCCACTTAAGGAGGCTTTTGAATGCAATAAACTAATAGTAGTGGCTAAA 303
          | |||| | | | | | | | | | | | | | | | | | | | | | | | |
Db       572  ATTATAAGGTTAATCATTTATATTCTAAATATATCATCATAGATATTAATTGATTAG 513
          | |||| | | | | | | | | | | | | | | | | | | | | | | | |
QY      304  ATTGTTAGTCAAAATTAATCTAGCTAACAAATAGCTACCTAACTATTAACTAATTTACCAA 363
          | |||| | | | | | | | | | | | | | | | | | | | | | | | |
Db       512  GTTTTTGTGATGTAATGTAGTCATTCAAATCCAAATTAATTAATTTATCATCAA 453
          | |||| | | | | | | | | | | | | | | | | | | | | | | | |
QY      364  AATAACTTATAGTAAATTAATTA 386
          | |||| | | | | | | | | | | | | | | | | | | | | | | | |
Db       452  AATACTATCGTTTTTAATTAATAA 430
          | |||| | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 11
US-09-601-198-3/c
; Sequence 3, Application US/09601198
; Patent No. 6531583
; GENERAL INFORMATION:
; APPLICANT: Cassell, Gail H.
; APPLICANT: Chen, Ellison Y.
; APPLICANT: Glass, Jennifer S.
; APPLICANT: Glass, John I.
; APPLICANT: Heiner, Cheryl R.
; APPLICANT: Lefkowitz, Elliot
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
; TITLE OF INVENTION: UREALYTICUM
; FILE REFERENCE: UAB-13452/22
; CURRENT APPLICATION NUMBER: US/09/601,198
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/073,189
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1308
; TYPE: DNA
; ORGANISM: Ureaplasma urealyticum
US-09-601-198-3

```

	Query Match	4.2%	Score 38.6;	DB 4;	Length 1308;
	Best Local Similarity	49.7%;	Pred. No. 0.22;		
	Matches	98;	Conservative	0;	Mismatches 99; Indels 0; Caps 0;
QY	283	ACTAATAGTTAGTGGCTAAAAATTTGTTAGTGAATATCTAGCTACAAATAGCTACCTA	342		
db	1203	AATAACCTTTTGTTTATTAAACACATTAAGAATATGCTTAACTCATTTATTTTGTGAT	1144		

QY	343	ACATTAACAAATTTACCAAAAAATAACTTATAAGTTAAATTAATTAAGTTGGCGTGTGTAA	402
Db	1143	ATTACITTCCTAAATCATCTAAAAATAACATCAGCATTTAAAAATCATATTCATATATTTAA	1084
QY	403	TGCTCAACTAAATTTTAGCCACCTAACTTTTATCTTTAGTGCATTTCAAAATGGCATAAGT	462
Db	1083	AGTTTCAATTTTGGCTAACAAATTTGTGTTTTCATTTTCGTTTAAAAATATCAAAATA	1024
QY	463	CTACGTTTGAATTTGAGA	479
Db	1023	AACAGCATAATTTGAAA	1007

```

RESULT 12
US-09-424-283-5/c
; Sequence 5, Application US/09424283
; Patent No. 6437219
; GENERAL INFORMATION:
; APPLICANT: Grimes, et al.
; TITLE OF INVENTION: Sucrose binding proteins
; FILE REFERENCE: 4630-50206
; CURRENT APPLICATION NUMBER: US/09/424,283
; CURRENT FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: PCT/US98/10465
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: US 60/047,568
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1924
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (119)..(1588)
US-09-424-283-5

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```

Query Match      4.1%;   Score 38.2;  DB 4;   Length 1924;
Best Local Similarity 84.3%;   Pred. No. 0.32;
Matches 43;  Conservative 0;  Mismatches 8;  Indels 0;  Gaps 0;

QY  1  ACTATAGGCACGCGTGGTCGACGCCCGGGCTGTCGATTATTGTGCCAA  51
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  1800  ACTATAGGCACGCGTGGTCGACGCCCGGGCTGTCGATTATTGTGCCAA  1750

```

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RESULT 13
US-09-570-367C-1/c
; Sequence 1, Application US/09570367C
; Patent No. 6338851
; GENERAL INFORMATION:
; APPLICANT: Gorczynski, Reginald M.
; TITLE OF INVENTION: Methods and Compositions for Immunomodulation
; FILE REFERENCE: 9579-21
; CURRENT APPLICATION NUMBER: US/09/570,367C
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/064,764
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2791
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-570-367C-1

```

Query Match 4.1%; Score 38; DB 4; Length 2791;
Best Local Similarity 89.1%; Pred. No. 0.43;
Matches 41; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 ACTATAGGCACGCGTGTGACGCCCGCGGTGCTGATTGTG 46

```

Db      2791 ACTATAGGACGGCTGGTCGACGCCCGGGCTGCTGCTAGTG 2746
|||||
RESULT 14
US-08-905-223-37
; Sequence 37, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESS: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 555 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: DOUBLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: Genomic DNA
; FEATURE:
; NAME/KEY: promoter
; LOCATION: 1..500
; FEATURE:
; NAME/KEY: transcription start site
; LOCATION: 501
; FEATURE:
; NAME/KEY: TF binding-site
; LOCATION: 191..206
; IDENTIFICATION METHOD: matinspector prediction
; OTHER INFORMATION: name ARNT_01
; OTHER INFORMATION: score 0.964
; OTHER INFORMATION: sequence GGACTCAGCTGCTGCT
; FEATURE:
; NAME/KEY: TF binding-site
; LOCATION: 193..204
; IDENTIFICATION METHOD: matinspector prediction
; OTHER INFORMATION: name NMVC_01
; OTHER INFORMATION: score 0.965
; OTHER INFORMATION: sequence ACTCAGCTGCTG
; FEATURE:
; NAME/KEY: TF binding-site
; LOCATION: 193..204
; IDENTIFICATION METHOD: matinspector prediction
; OTHER INFORMATION: name USF_01
; OTHER INFORMATION: score 0.985
; OTHER INFORMATION: sequence ACTCAGCTGCTG
; FEATURE:
; NAME/KEY: TF binding-site

```

```

; LOCATION: complement(193..204)
; IDENTIFICATION METHOD: matinspector prediction
; OTHER INFORMATION: name USF_01
; OTHER INFORMATION: score 0.985
; OTHER INFORMATION: sequence CAGCAGCTGAGT
; FEATURE:
; NAME/KEY: TF binding-site
; LOCATION: complement(193..204)
; IDENTIFICATION METHOD: matinspector prediction
; OTHER INFORMATION: name NMVC_01
; OTHER INFORMATION: score 0.956
; OTHER INFORMATION: sequence CAGCAGCTGAGT
; FEATURE:
; NAME/KEY: TF binding-site
; LOCATION: complement(193..204)
; IDENTIFICATION METHOD: matinspector prediction
; OTHER INFORMATION: name MYCWX_02
; OTHER INFORMATION: score 0.972
; OTHER INFORMATION: sequence CAGCAGCTGAGT
; FEATURE:
; NAME/KEY: TF binding-site
; LOCATION: 195..202
; IDENTIFICATION METHOD: matinspector prediction
; OTHER INFORMATION: name USF_C
; OTHER INFORMATION: score 0.997
; OTHER INFORMATION: sequence TCACGTGC
; FEATURE:
; NAME/KEY: TF binding-site
; LOCATION: complement(195..202)
; IDENTIFICATION METHOD: matinspector prediction
; OTHER INFORMATION: name USF_C
; OTHER INFORMATION: score 0.991
; OTHER INFORMATION: sequence GCACGTGA
; FEATURE:
; NAME/KEY: TF binding-site
; LOCATION: complement(210..217)
; IDENTIFICATION METHOD: matinspector prediction
; OTHER INFORMATION: name MZFI_01
; OTHER INFORMATION: score 0.968
; OTHER INFORMATION: sequence CATGGGGA
; FEATURE:
; NAME/KEY: TF binding-site
; LOCATION: 397..410
; IDENTIFICATION METHOD: matinspector prediction
; OTHER INFORMATION: name ELK1_02
; OTHER INFORMATION: score 0.963
; OTHER INFORMATION: sequence CTCCTCGGAAGCCT
; FEATURE:
; NAME/KEY: TF binding-site
; LOCATION: 400..409
; IDENTIFICATION METHOD: matinspector prediction
; OTHER INFORMATION: name CETS1F54_01
; OTHER INFORMATION: score 0.974
; OTHER INFORMATION: sequence TCCGGAAGCC
; FEATURE:
; NAME/KEY: TF binding-site
; LOCATION: complement(460..470)
; IDENTIFICATION METHOD: matinspector prediction
; OTHER INFORMATION: name APL_Q4
; OTHER INFORMATION: score 0.963
; OTHER INFORMATION: sequence AGTGACTGAAC
; FEATURE:
; NAME/KEY: TF binding-site
; LOCATION: complement(460..470)
; IDENTIFICATION METHOD: matinspector prediction
; OTHER INFORMATION: name APLFJ_Q2
; OTHER INFORMATION: score 0.961
; OTHER INFORMATION: sequence AGTGACTGAAC
; FEATURE:
; NAME/KEY: TF binding-site
; LOCATION: 547..555
; IDENTIFICATION METHOD: matinspector prediction
; OTHER INFORMATION: name PADS_C

```

```
;
; OTHER INFORMATION: score 1.000
; OTHER INFORMATION: sequence TGTGTCGTC
US-08-905-223-37

Query Match
Best Local Similarity 4.1%; Score 37.8; DB 3; Length 555;
Matches 39; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 CWTAGGGCACGGTGGTGCACGGCCGGGCTGTCGTATTGTG 46
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 CWTAGGGCACGGKTTGTCGACGGCCGGGCTGTCGTGTCGTG 45

RESULT 15
US-09-247-155-37
; Sequence 37, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET 021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 37
; LENGTH: 555
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: promoter
; LOCATION: 1..500
; FEATURE:
; OTHER INFORMATION: codon_start="501"
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: 191..206
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name ARN1_01
; OTHER INFORMATION: score 0.964
; OTHER INFORMATION: sequence ggactcacgtgtgtgct
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: 193..204
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name NMVC_01
; OTHER INFORMATION: score 0.965
; OTHER INFORMATION: sequence actcaactgtgtg
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: 193..204
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name USF_01
; OTHER INFORMATION: score 0.985
; OTHER INFORMATION: sequence actcacgtgtgctg
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: complement(193..204)
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name USF_01
; OTHER INFORMATION: score 0.985
; OTHER INFORMATION: sequence cagcacgtgagtg
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: complement(193..204)
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name NMVC_01
; OTHER INFORMATION: score 0.956
; OTHER INFORMATION: sequence cagcacgtgagtg
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: complement(193..204)
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name MYCAX_02
; OTHER INFORMATION: score 0.972
; OTHER INFORMATION: sequence cagcacgtgagtg
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: 195..202
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name USF_C
; OTHER INFORMATION: score 0.997
; OTHER INFORMATION: sequence tcaactgtgc
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: complement(195..202)
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name USF_C
; OTHER INFORMATION: score 0.991
; OTHER INFORMATION: sequence gcaactgtga
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: complement(210..217)
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name MZFL_01
; OTHER INFORMATION: score 0.968
; OTHER INFORMATION: sequence catgggga
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: 397..410
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name ELK1_02
; OTHER INFORMATION: score 0.963
; OTHER INFORMATION: sequence ctctccggaagcct
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: 400..409
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name CETSIP54_01
; OTHER INFORMATION: score 0.974
; OTHER INFORMATION: sequence tccggaagcc
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: complement(460..470)
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name API_04
; OTHER INFORMATION: score 0.963
; OTHER INFORMATION: sequence agtgactgaac
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: complement(460..470)
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name APIFJ_02
; OTHER INFORMATION: score 0.961
; OTHER INFORMATION: sequence agtgactgaac
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: 547..555
; OTHER INFORMATION: matinspector prediction
; OTHER INFORMATION: name PADS_C
; OTHER INFORMATION: score 1.000
; OTHER INFORMATION: sequence tgtgtgtctc
; US-09-247-155-37

Query Match 4.1%; Score 37.8; DB 4; Length 555;
Best Local Similarity 86.7%; Pred. No. 0.26;
US-09-247-155-37
```

Matches	39;	Conservative	2;	Mismatches	4;	Indels	0;	Gaps	0;
Qy	2	CTATAGGGCACGCTGGTCGACGCGCCCGGCTGGTCGTAATTTGTG	46						
Db	1	CTATAGGGCACGCTGGTCGACGCGCCCGGCTGGTCGTAATTTGTG	45						

Search completed: October 17, 2003, 10:50:08
 Job time : 67 secs